Ősrégészeti Tanulmányok / Prehistoric Studies

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MOMENTS IN TIME

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Series Editors

Alexandra Anders, Gábor Kalla, Viktória Kiss,
Gabriella Kulcsár and Gábor V. Szabó

MOMENTS IN TIME

Papers Presented to Pál Raczky on His 60th Birthday

Edited by

Alexandra Anders and Gabriella Kulcsár

with

Gábor Kalla, Viktória Kiss and Gábor V. Szabó

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Interdisciplinary Archaeology

Domesticating Mathematics: Taxonomic Diversity in Archaeozoological Assemblages

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Understanding taxonomic richness is indispensable in studying the choices made in the exploitation of the local fauna such as those of the broad-spectrum revolution in the Near East. Such investigations, however, sometimes disregard the stochastic nature of human decision-making, while others present complex mathematical models. The basic nature of samples is rarely discussed.

The fundamental thesis of our study is that assemblages of different sizes can be compared only exercising extreme caution. When species richness is studied as a function of assemblage size, the remains of birds, large and "micro-" mammals show strongly differing statistics. Diversity increases along with the number of identifiable bones in the case of birds, while the same trend is most protracted in the case of large mammals. This means that taxonomic diversity in animal bone assemblages is a function of not only assemblage size but also of taxonomic composition. The structure of "input" data is thus qualitatively dependent on assemblage size.

The underlying factors influencing the archaeological representation of the fauna, including sampling, anatomical and taphonomic traits of the three types of vertebrates are discussed by animal groups. Taxonomically different animal remains should not be included within the same faunal list as their culture historical interpretations (animal keeping, hunting, random natural deposition) also differ. These phenomena must all be considered when a reliable interpretation of animal remains is attempted in various archaeological periods.

A régészeti állatcsont-anyagok fajgazdagságának megértése nélkülözhetetlen olyan kérdések kutatásában, mint pl. a közel-keleti őskori közösségek által fogyasztott állatfajok rendszertani spektrumának szélessége, választékának kihasználása. Az ilyen vizsgálatok során sokan figyelmen kívül hagyják az emberi döntések sztochasztikus természetét, míg mások bonyolult matematikai modellekkel igyekeznek leírni azt. A minták alapvető természetére kevesen fordítanak figyelmet.

Vizsgálataink alaptétele, hogy a különböző nagyságú minták csak rendkívüli körültekintéssel hasonlíthatók össze. Amikor a meghatározott fajok számát a mintanagyságok függvényében vizsgáljuk, a madarak, a nagytestű emlősállatok és a „mikrofauna" emlős fajai más-más értékeket mutatnak. A fajgazdagság nem lineárisan követi a csontok darabszámának alakulását: ahhoz viszonyítva a madarak esetében növekszik a legintenzívebben, leginkább pedig a nagytestű emlősök csoportjában marad el a mintanagyság gyarapodásától. Eszerint az egyes leletegyüttesek állattani változatossága nemcsak a mintanagyságtól, hanem a taxonómiai összetételtől is függ. Ez azt mutatja, hogy a régészeti értelmezésben már a „bejövő" alapadatok összetétele is minőségileg függ a mintanagyságtól.

A tanulmányban körvonalazzuk a háttérben meghúzódó okokat, a három vizsgált gerinces állatcsoport reprezentáltságát meghatározó mintavételi, tafonómiai és anatómiai különbségeket. E maradványok értelmezése nem mosható egybe egyetlen „faunalistában", hiszen kultúrtörténeti jelentésük (állattartás/vadászat, madarászat és véletlenszerű, természetes lerakódás) is változó. Mindez nem mellőzhető az állatok különböző régészeti korszakokban játszott szerepének hitelességre törekvő értékelésekor.

INTRODUCTION

According to its internationally accepted definition, "archaeozoology… is the study of the relationships between humans and non-human animals over time. It usually involves the study of animal remains… from archaeological sites" (ICAZ n. d.). In addition, archaeozoology has played an important role in reconstructing ancient environments around archaeological sites. An in-depth, functional understanding of taxonomic diversity in faunal assemblages is indispensable in testing hypotheses concerning important concepts such as the Broad Spectrum Revolution put forward by Kent Flannery (1969) implying that the emergence of the Neolithic throughout Southwest Asia was prefaced by increases in "dietary breadth" among foraging societies. Hunting, animal husbandry and fishing are habitually discussed especially in prehistoric archaeology that tends to define itself as a scientifically informed discipline in contrast to "historical archaeology" whose experts often tend to be less enthusiastic about using scientific methodology.

The use of mathematics in solving these problems varies between extremes in archaeozoology. It ranges from the complete ignorance of the fact that human behaviour has been stochastic in nature since the earliest times, to extremely complex theoretical models that remain intangible in the absence of proper field data. In archaeozoology routine applications of simple mathematics include the estimation of withers heights of animals that has raised only minute excitement in the community of archaeologists and the calculation of meat weights often based on the contradictory minimum numbers of individuals (MNI), whose end results sold well to unsuspecting outsiders, but are laden with uncontrollable, cumulated bias. The most important of these is that the exact time period during which the estimated amounts of meat were consumed remains unknown, making the results completely fictional (Guilday 1970).

Meanwhile, there would be plenty of room left for the more precise assessment of the nature of archaeozoological assemblages prior to culture-historical interpretation. We know for sure that the find material is incomplete and its composition is the outcome of a host of taphonomic processes. Their destructive effect depends on the nature of the medium (i. e. animal remains), context (i. e. circumstances of deposition) and interpretation (i. e. methods of recovery, identification and analysis). All three have quantitative aspects of decisive importance, as sample size determines the reliability of our conclusions. This phenomenon is analogous with the principle of allometry in biology, the study of relative growth, of changes in proportion with increase in size (*Fig. 1*; Huxley 1932). Should the general principle of growth be applicable to archaeozoological assemblages, we could develop a better understanding of how increasing sample size would effect the proportion between its various components, much the same way as the shape and body composition of an animal changes with size.

THE PROBLEM

Animal husbandry and hunting practices changed through time and the anthropogenic impact had feed-back effects on the environment (Bartosiewicz 2005). In order to reconstruct gross diachronic trends in archaeology, bone assemblages from numerous sites need to be comparable. It has been demonstrated that — until a certain point — the number of animal species recognized in

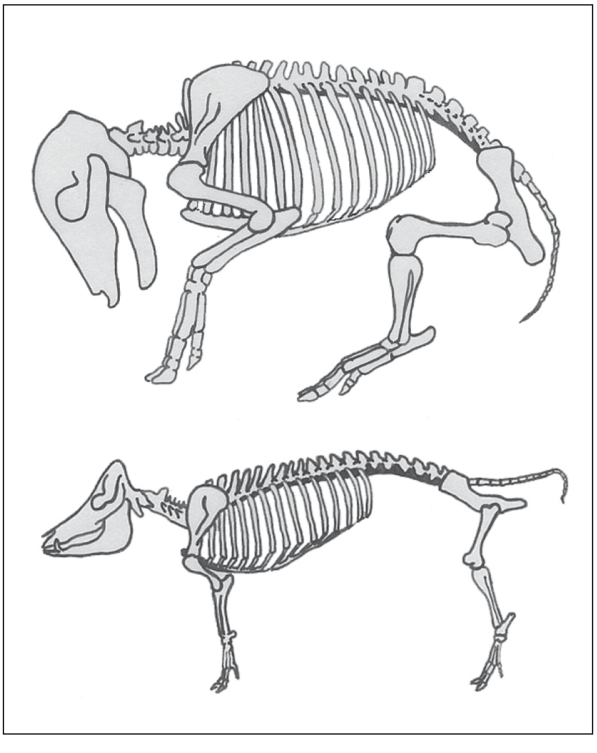

Fig. 1. Allometry: sketch of a *foetal* (top) and *adult* pig skeleton, showing how proportions change along with growth (after Huxley 1932)

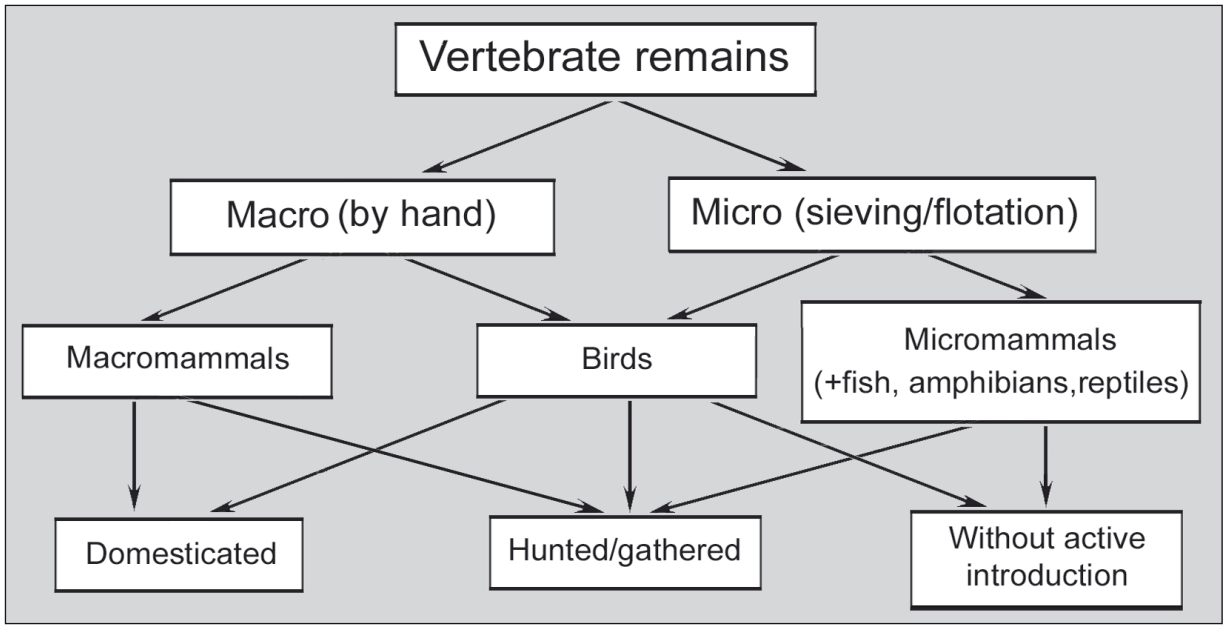

Fig. 2. Relationships between the mode of recovery, taxonomy and archaeozoological interpretation

an assemblage (R: taxonomic richness) increases along with the number of identifiable bone specimens (NISP). It is for this reason that comparisons between faunal assemblages of radically different sizes can be heavily biased, since the number of species would rather reflect the number of bones available for the researcher (Grayson 1984, 136–137) than the subject of archaeozoology: the culturally idiosyncratic composition of animal taxa exploited by ancient communities.

The interpretation of this quantitative tendency, however, is further complicated by the fact that in the archaeozoological literature animal species from all vertebrate classes (and sometimes even molluscs) tend to be pooled in calculations, and little attention is paid to fundamental taxonomic and taphonomic differences that may affect the results. It has become clear, that different vertebrate classes show tremendous variability in terms of preservation, recovery and archaeological interpretation, partly related to quantitative features of their anatomy. The relationships between species richness and samples size in mammalian and avian bone assemblages were studied by László Bartosiewicz and Erika Gál (2007). In the present article this comparison is further extended to include micro-mammals. We tried to determine the various sources of bias that may distort comparisons between the representation of three types of animal remains (macro-, micromammals and birds) in the archaeological record.

During archaeological excavations, animal remains may be collected in two basic ways. Large bone fragments are gathered by hand while most small bones can be retrieved only using flotation and/or sieving of soil samples *(Fig. 2)*. The two size classes recovered by the different methods correspond to the gross group of macro- and microfaunal finds. In this study, mammals over 5000 g live weight are considered macromammals while below this value they are classified as micromammals. In that way we counted among macromammals the hare *(Lepus europaeus)*, rabbit *(Oryctolagus domesticus)* and European rabbit *(Oryctolagus cuniculus)*, beaver *(Castor fiber)*, common otter *(Lutra lutra)* and badger *(Meles meles)*.

Analyzing the hand-collected assemblage of macromammals and large birds, information is gained concerning hunting and animal husbandry practices as reflected by the mode of consumption of the sites' past inhabitants. These assemblages are heavily influenced by human action; the environmental reconstruction is biased by anthropogenic noise (Bartosiewicz 2001). However, the water-sieving and/or flotation of soil samples yields additional microvertebrate remains. Although some of these animals may have been exploited by humans (e. g. hamsters were skinned; Bartosiewicz 2003, 115, Fig. 14; fish could be caught actively or gathered in residual flood pools) the majority of microfauna (amphibians, reptiles, micro-mammals) ended up in ancient deposits without active

human introduction. They were often attracted by food sources or nesting opportunities within the human habitat.

In spite of their increasing interference with nature, humans have exploited only a fraction of the species represented in the natural fauna of their environments. It is poorly understood why only some two dozen animal species were domesticated (Gentry–Clutton-Brock–Groves 2004), and even the choice of hunted game tends to be relatively limited. The micromammals contribute valuable complementary information to reconstructing the environment, as studying their naturally deposited sub-assemblages can balance for the selective effect of ancient human activity that usually disregarded economically insignificant but ecologically diagnostic animals. Species composition is an indicator of habitats in the settlement's area, since various rodents and insectivores are diagnostic of different types of vegetation and thus different environmental conditions. Numerous species in the microfauna, as well as several birds, are commensal, meaning animals that have not been domesticated, but are "eating together" with humans, i. e. have become dependent on their habitat (e. g. mice, rats, sparrows, crows). Based on the presence of such synanthropic species more information can be obtained concerning the use of various settlement features (for example cereal storage facilities, rubbish pits etc.).

Even in the case of micromammals only a fraction of the original fauna is available for reconstructing the environment of a settlement and its inhabitants' way of life. Animal remains undergo many *post mortem* taphonomic changes which decimate the bone assemblage. From the mode of hunting and production practices of the inhabitants to excavation techniques there are many effects reducing the assemblages.

MATERIALS

Thirty-five of the 53 macromammalian samples from Neolithic and Copper Age sites reviewed recently (Bartosiewicz 2005, Table 6. 1) have been selected for this study to be compared to 29 bird bone assemblages that range from the Early Neolithic through the Bronze Age. Archaeo-ornithological research during recent years in Hungary and Romania has offered a unique opportunity to compare several avian and mammalian bone assemblages from the Neolithic and Chalcolithic in the region (Gál 2007a, 62, Fig. 9 and 65, Fig. 10). Some of these data had already been available in the literature (Bökönyi–Jánossy 1965; Jánossy 1985; Bökönyi 1992; Gál 2004; Pike-Tay et al. 2004; Gál 2006; 2007b). Unpublished avian assemblages used in this paper include those from Balatonkeresztúr-Réti-dűlő (Copper and Bronze Ages), Balatonszemes-Bagódomb (Copper and Bronze Ages), Felsővadász-Várdomb (Neolithic and Bronze Age), Ordacsehi-Kistöltés (Bronze Age–Iron Age transition). There are few known micromammalian assemblages from archaeological sites (especially from open air sites) from Hungary because flotation or water-sieving were almost unknown to archaeologists (Bartosiewicz 1988). Therefore we had to use micromammalian samples from a wider chronological interval — from the Mesolithic to the Roman period — in order to obtain a viable sample size. Bones from altogether twenty sites were collected for this analysis. Only a small fraction (4 sites) was published in the literature (Jánossy–Kordos 1976; Kordos 1987a; Domokos–Kordos–Krolopp 1989). Eight samples were identified by the third author of this paper and will be published in her thesis, while seven were studied and documented by László Kordos in the "grey literature" (Kordos 1980–81; 1981; 1982a; 1982b; 1983; 1987b; 1991a; 1991b). All avian and large mammalian samples come from open-air sites while three of the micro-mammalian samples originate from cultural deposits in caves.

There is a notable cultural difference between macromammalian and avian assemblages since one may reckon with the presence of at least five domesticates among mammals (the "Neolithic package" of dog, sheep, goat, cattle, pig and possibly even horse by the Bronze Age), while prehistoric bird bone assemblages, pre-dating the occurrence of domestic fowl in the Carpathian Basin, represent exclusively wild species.

METHODS

Comparing relative frequencies in terms of percentages is a widely practiced method in the quantitative analysis of archaeological assemblages of all sorts. It is well known, however, that in the absence of sufficiently large samples of representa-

Vertebrate group	Number of sites	Coefficients of			Level of probability
		regression	integration	determination	
Macromammal	35	0.174	0.568	0.692	0.010
Micromammal	20	0.321	0.365	0.707	0.000
Bird	29	0.571	0.020	0.750	0.000

Table 1. Parameters of linear equations for macro- and micromammalian as well as avian assemblages shown in *Figure 3*

tive value no reliable conclusions can be drawn. Rare finds occur in small samples with far smaller probability. When they do, however, they look disproportionately overrepresented in percentual terms, illustrating the crucial importance of sufficiently large assemblage sizes.

The relationship between assemblage size (NISP) and the number of taxa identified (taxonomic richness: R) may be studied in a straightforward manner using regression analyses easily illustrated in bivariate plots. Although there is a usually high, positive correlation between the number of identifiable bones and taxonomic richness, this relationship is not linear: the number of species follows increasing sample size in a degressive manner and is "exhausted" when new species are no longer encountered in the assemblage. In the theoretical case of perfectly random sampling, the rarest species would be the last to occur. This trend can be described by fitting exponential curves to the data points.

Exponential equations, however, are difficult to compare. The heteroscedasticity of our data, i. e. taxonomic variability increasing by absolute assemblage size has therefore been reduced by using decimal logarithms of both NISP and R in calculating regression equations between the two variables for the three groups of vertebrates analyzed in this study, macro- and microvertebrates and birds. The logarithmic transformation results in linear regression equations that lend themselves to easier interpretation. In the resulting graph the distribution of data points is more even and the trends characteristic of the two mammalian and bird bone assemblages may be compared more conveniently.

RESULTS

Parameters of the regression lines calculated for the three animal groups are listed in *Table 1*, while the bivariate plots and relevant trend lines are shown in *Figure 3*.

The most striking difference between the three vertebrate groups is shown between the slope of their respective trend lines, that is the coefficients of regression obtained that is also immediately visible in *Figure 3*.

There is a more than threefold difference between the value characteristic of bird and macromammalian assemblages reveals that significantly fewer bones from birds result in the occurrence of new species. In other words, the trend of increasing taxonomic richness is less degressive in the case of avian remains, i. e. sample size is more worth increasing than for macromammalian samples. Taxonomic, anatomical and taphonomic explanations for these extermes have been outlined by L. Bartosiewicz and E. Gál (2007). These points are reconsidered here in light of the new results on micromammals.

The equation and regression line obtained for micromammals fall almost exactly between the

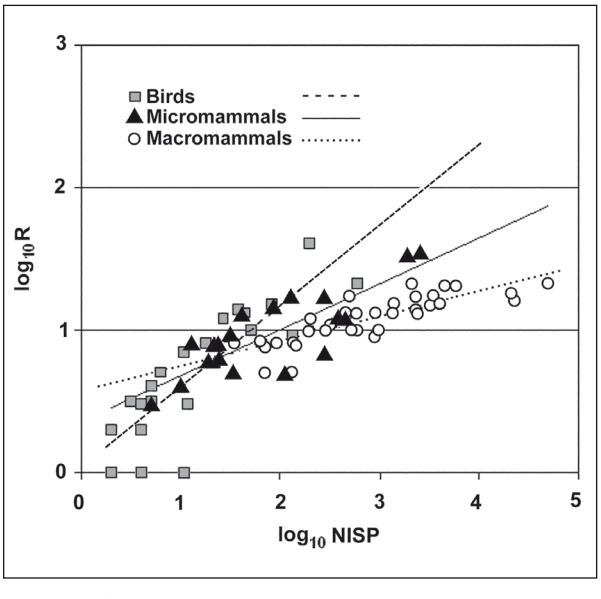

Fig. 3. Differences between the trends by which the number of taxa (R) increases as a function of assemblage size (NISP) in birds, micro- and macromammals

	Macroammals	Micromammals	Birds
Known modern fauna	42	70	363
Archaeological evidence	34	57	93
Percent of representation	80%	68%	26%

Table 2. The number of macro- and micromammalian and avian species

extreme trends outlined for macromammals and birds. Increasing sample sizes in this group yield new species at a faster rate than in macromammals, but they fall short of the spectacular increase characteristic of birds.

Differences in the coefficient of integration (intersection point with the y axis representing taxonomic richness) indicate that there is a smaller rate of increase to be reckoned with in mammalian bone assemblages. Coefficients of determination show close, statistically significant relationships between the two variables in all three groups of assemblages. We can predict taxonomic richness equally well in both groups, but it will increase most rapidly along with assemblage size in the case of birds, then micromammals and finally macromammals.

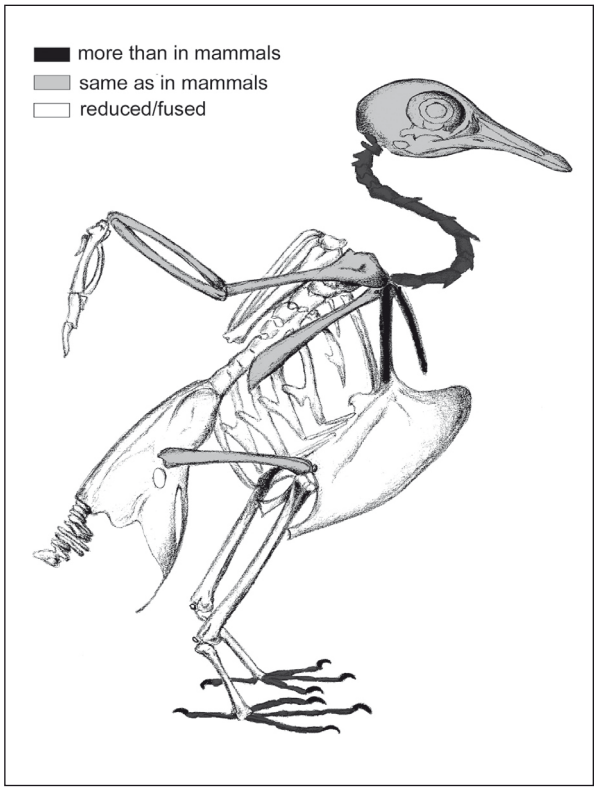

Fig. 4. Bird skeleton showing the number of bones in comparison with those in the generalized mammalian skeleton. (Drawing A. Biller)

DISCUSSION

The taxonomic explanation for this trend is that in the modern (holocene) fauna of Hungary, one may reckon with more micromammalian species than macromammals (the latter including domesticates; Rakonczay 1990; Ujhelyi 1994; Vörös 2003). Micromammalian taxa identified at archaeological sites also tend to outnumber those of macromammals. This is related to the evident fact that the number of usually dominant domestic animals is complemented only by a relatively small number of wild animal species. When the number of animal taxa known from archaeological excavations is comapred to the total number in the modern fauna the following proportions can be established *(Tab. 2)*.

The special anatomy of birds, adapted to flying also offers partial explanation for the very steep regression line obtained for this class of vertebrates. Main differences compared to the skeleton of mammals originate from bipedal walking and specialization to flying. The latter is especially expressed in the decreased number of skeletal parts and the fusion between several bones, a structural phenomenon stabilizing the body during flight *(Fig. 4)*. Birds have more *cervical vertebrae* (11–23) than mammals (7). *Thoracic vertebrae* are fused. The last *thoracic vertebra*, the single *lumbar vertebra* and the *sacral vertebrae* and the pelvis form the *synscacrum*. The last caudal vertebrae form the *pigostyl*. The *coracoideum, scapula* and *clavicula* (wishbone) of the pectoral girdle are all fused into the scapula in quadrupedal mammals. In the wing, there are only two *carpal* bones (*cubitale* and *radiale*), the rest are fused into the *carpometacarpus* which includes the fused carpals and the 2nd–4th metacarpals. In the feet, the first row of tarsals is fused to the distal part of *tibia*, called therefore the *tibiotarsus*. The *tarsometetarsus* is composed of the distal tarsal bones fused onto the proximal end of the fused 2nd–4th metatarsals (see *Fig. 5*). Most of bird

species have only four digits in the feet, but numerous phalanges.

As a result of these features, one may reckon only with 75–100 individual bones in a complete avian skeleton, depending on the number of cervical vertebrae and ribs, if the skull is counted as a single bone. Mammalian skeletons, on the other hand, are composed of approximately 200 elements on average, when the skull and *pelvis* are counted as single bones. Only relatively minor differences are caused by the different degrees of fusion in the foot. Otherwise the number of bones is exactly the same in the skeleton of a squirrel and a pig. While the number of cervical vertebrae is constant (7) complex articulations that aid locomotion on ground (especially between vertebrae and in the *carpal* and *tarsal* joints), increase the weight of mammals in comparison with birds *(Fig. 5)*. Differences between the resistivities of mammalian and avian bones are also largely density-mediated *(Fig. 6)*.

In spite of the near-identity of macro- and micromammals in terms of the number of skeletal elements, an overwhelming majority (88%) of the lapper can be identified to species exclusively on the basis of the skull and mandibles, some only in the presence of teeth. Other bones of limited use include the *scapula, humerus, ulna, radius, pelvis, femur, tibia*). This is in sharp contrast with macromammals whose vertebrae and extremity bones can also be routinely identified. The inevitable identification bias in micromammals "reduces" the number of taxonomically diagnostic skeletal elements that determine species richness. Therefore there is an artificial "similarity" between the anatomy of the bird and micromammalian skeleton that results in the steeper, more "bird-like" slope of their regression line in *Figure 3*.

Finally, the different taphonomy of micromammals must also be considered. Both the number of species available and the aforementioned structural traits of the skeletons influence the archaeological representation of macro- and micromammals as well as birds through a filter of various stages in the taphonomic process that determine the final composition of archaeozoological assemblages. Similarly to those of birds, the small bones of micromammals are far less prone to intensive fragmentation than the large skeletal remains of macromammals, also frequently damaged by intentional butchering. In the latter case, NISP is disproportionally increased by various parts of the same bone being identified and counted separately (without recognizing the relation between its fragments). The bones of micromammals and birds on the other hand, are not overrepresented this way that creates one more similarity behind their regression lines.

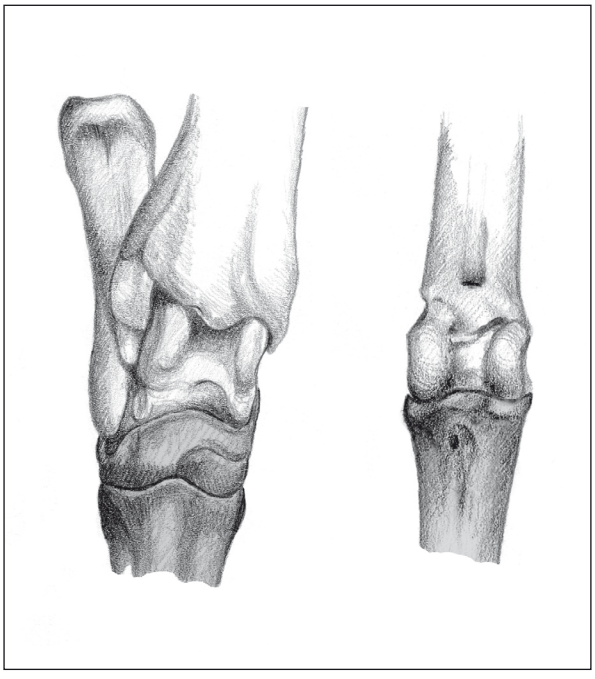

Fig. 5. Distal end of the tibia with tarsal bones in a mammal (*Artiodactyl*; left) compared to the distal end of a bird *tibiotarsus* (right). The separate *calcaneus* and *astragalus* (light shading) in mammals are fused to the tibia in birds. Separate tarsal bones in the lower row in mammals (dark shading) are articulated with the metatarsus in birds. (Drawing A. Biller)

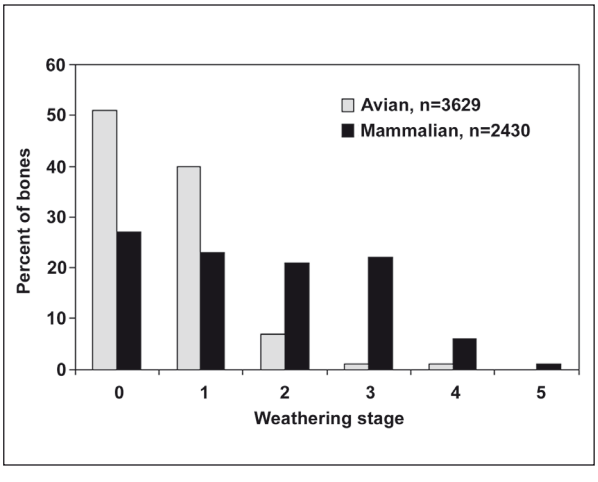

Fig. 6. Comparison between bones in different weathering stages for birds and mammals in samples from Patagonia (after Cruz 2008, 34, Fig. 3)

CONCLUSIONS

Animal exploitation in prehistory involved a number of decisions, beginning with the choice of animals to be culled or hunted as well as the natural accumulation of bones from commensal animals in archaeological deposits. Most of the latter belong to the microfauna that was compared to assemblages of larger bones from macromammals and birds. Evidently, access to various taxa differed broadly between animal keeping, terrestrial hunting, fowling and fishing in addition to the contribution of this natural element. The fauna of the habitat within which humans settled, therefore, is reflected selectively in archaeological assemblages (Bartosiewicz 2001).

In this paper, studies of this selectivity could be carried one step further. For various reasons (taxonomic, anatomical and taphonomic) the number of taxa increases differently between macro- and micromammals and birds. Recalling the principle of allometry mentioned in the introduction to this paper, it means that taxonomic richness, directly dependent on sample size in all three groups of animal remains, will also show differential growth as a function of assemblage size. When only smaller quantities of zoological find material are available for study, birds and micromammals will be disproportionally underrepresented. On the other hand large assemblages, very monotonous in terms of macromammals whose basic species may be present in smaller samples, will still offer new bird and micromammalian species with great probability.

The importance of considering these differences from an archaeological point of view is that through sample size, they have a direct impact on the interpretation of animal remains. The use of large assemblages as well as familiarity with such qualitative detail may help better understanding ancient lifeways and shed light on the relationships between animal keeping, hunting and fowling, whose studies require different methods and can therefore be integrated only within a relatively loose interpretational framework.

Last not but least, these important trends could be revealed using relatively simple statistics: linear regression analysis was applied to this problem following analogous use in allometric calculations in biology. It must be emphasized, however, that many of these details would have been masked by the simplistic percentual evaluation of faunal lists that often tends to disregard assemblage sizes and becomes outright misleading when the pooled remains of macro- and micromammals together with birds are taken as the 100% base unit.

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